

GenCore version 5.1.3
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OW protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2002, 03:34:15 : Search time 57 Seconds
(without alignments)
2835.415 Million cell updates/sec

Title: US-09-784-340-2
Perfect score: 2802
Sequence: 1 MRSDKSLVFLQLQFCVGC.....KCFLESCQKFKRKIEKRE 527

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model DEV=xlh
-O=/cgn2_1/USPFO.spool/US09784340/runat_02122002_122447_18980/app_query.fasta_1.711
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blcosum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-WARN_TIMEOUT=30 -THRADE=0.1 -XGAPOP=10 -XGAPEXT=0.5 -FPGAPOP=6 -FPGAEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued_Patents_NA:*
2: /cgn2_6/plodata/1/ina/5A.COMB.seq:*
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5: /cgn2_6/plodata/1/ina/6B.COMB.seq:*
6: /cgn2_6/plodata/1/ina/PCtus.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	61.8	2107	4	US-09-180-852-1
2	1399	49.9	1413	4	US-09-813-918-1
3	1131	40.4	2336	5	PCT-US92-00282-1
4	1068.5	38.1	2339	5	PCT-US92-00282-2
5	391	14.0	391	4	US-09-370-838-21
6	377.5	13.5	1190	5	PCT-US92-00282-18
7	318.5	11.4	1448	5	PCT-US92-00282-16
8	317.5	11.3	1008	5	PCT-US92-00282-10
9	297	10.6	1066	5	PCT-US92-00282-14
10	287	10.2	783	5	PCT-US92-00282-22
11	281.5	10.0	1561	5	PCT-US92-00282-25
12	274.5	9.8	2025	4	US-08-942-0128-23

13	272.5	9.7	1219	5	PCT-US92-00282-8	Sequence 8, Appli
14	271.5	9.7	1197	5	PCT-US92-00282-12	Sequence 12, Appl
15	265	9.5	1800	6	5180581-1	Patent No. 5180581
16	265	9.5	2793	1	US-08-281-916-5	Sequence 5, Appl1
17	265	9.5	2793	1	US-08-460-725-7	Sequence 7, Appl1
18	180	6.4	6918	1	US-07-783-705A-13	Sequence 13, Appl1
19	175	6.2	1296	1	US-07-783-705A-8	Sequence 8, Appl1
20	172.5	6.2	1200	1	US-08-096-633A-19	Sequence 19, Appl
21	168.5	6.0	8051	2	US-08-576-626A-2	Sequence 2, Appl1
22	158	5.6	1245	1	US-09-337-913-2	Sequence 2, Appl1
23	158	5.6	1245	1	US-08-750-524-2	Sequence 2, Appl1
24	154.5	5.5	50937	4	US-09-428-517-1	Sequence 1, Appl1
25	150	5.4	1607	2	US-08-797-226-1	Sequence 1, Appl1
26	147	5.2	1627	3	US-09-106-464-1	Sequence 1, Appl1
27	143.5	5.1	1669	2	US-08-522-421-1	Sequence 1, Appl1
28	141	5.0	1731	2	US-08-466-583-1	Sequence 1, Appl1
29	141	5.0	1731	1	PCT-US95-07820-1	Sequence 1, Appl1
30	129.5	4.6	1332	1	US-08-660-762A-3	Sequence 3, Appl1
31	124	4.4	762	4	US-09-615-192A-218	Sequence 218, App
32	122	4.4	513	5	PCT-US92-00282-20	Sequence 20, Appl
33	120.5	4.3	3756	2	US-08-576-626A-1	Sequence 1, Appl1
34	119.5	4.3	330	4	US-09-615-192A-168	Sequence 168, App
35	119.5	4.3	1738	2	US-08-379-482A-2	Sequence 2, Appl1
36	115.5	4.1	80161	3	US-09-036-987A-1	Sequence 1, Appl1
37	115.5	4.1	80161	4	US-09-370-700-1	Sequence 1, Appl1
38	111.5	4.0	1176	4	US-09-134-001C-1115	Sequence 1115, Ap
39	105.5	3.8	405	2	US-08-975-316-32	Sequence 32, Appl
40	105.5	3.8	405	4	US-09-615-192A-32	Sequence 32, Appl
41	105.5	3.8	479	4	US-09-615-192A-114	Sequence 114, App
42	104	3.7	87563	4	US-09-453-702B-57	Sequence 57, Appl
43	103	3.7	8657	4	US-08-961-527-44	Sequence 44, Appl
44	100	3.6	6826	3	US-09-024-020B-8	Sequence 8, Appl1
45	100	3.6	6826	4	US-09-425-043-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-180-852-1
Sequence 1, Application US/09180852
Patent No. 6287834
GENERAL INFORMATION:
APPLICANT: BELANGER, Alain
APPLICANT: HUM, Dean W.
APPLICANT: BEAULIEU, Martin
APPLICANT: LEVESQUE, Eric
TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
FILE REFERENCE: 1259-449
CURRENT APPLICATION NUMBER: US/09/180, 852
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: PCT/CA97/00328
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: US 08/649, 319
EARLIER FILING DATE: 1996-05-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2107
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(1644)
US-09-180-852-1
Alignment Scores:
Pred. No.: 3.53e-198
Score: 1732.00
Percent Similarity: 75.47%
Best Local Similarity: 61.51%
Query Match: 61.81%
DB: 4
Length: 2107
Matches: 326
Conservative: 74
Mismatch: 112
Indels: 18
Gaps: 3

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US-09-784-340-2 (1-527) x US-09-180-852-1 (1-2107)
Oy 9 ValPheLeuLeuGlnLeuPheCys---ValGlyCysGlyPheCysGlyLysValLeu 27
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Db 73 GCTCTTCGCTGATGACAGTCAGTTGACTTACCTGCGAGGTGGAAAGGTGCTG 132
Oy 28 ValTTPProCysAspMetSerHisTTPLeuAsnValLysValLLeuGlnLeuLe 47
    |||||.....|||
Db 133 GTGTGGCCCAAGCAATACAGCCATTGGATAATATGAACACATCTCTGGAGAGCTTGT 192
Oy 48 ValArgGlyHisGlyValThrValLeuThrHisSerLysProSerLeuLeaSPtyrArg 67
    |||||.....|||
Db 193 CAGAGGGGCTATGAGTGTATGTTGACATCTGCGCTTCTATCTGTGCAATGCCAGT 252
Oy 68 LysProSerAlaLeuLysPheGlyValValHisMetProGlnAspArgThrGlnGln 87
    |||||.....|||
Db 253 AATTCATCTGCTATTAATTAATGAACTTATCCTACATCTTAACTTAATAAATATTTGGA 312
Oy 88 GlnIlePheValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTTPGlnSerVal 107
    |||||.....|||
Db 313 GATTTTATATGAAATG-----TTGATATGATGAGCATATAGT 351
Oy 108 IleLysLeuAsnAspPhePheValGlnIleArgGlyThrLeuLysMet----- 123
    |||||.....|||
Db 352 ATTTCAAAAATATCATTTTGTGCTATTTTTCACAACTACAGAAATGTTGGGAAAT 411
Oy 124 -----MetCysGlnSerPheIleTyrAsnGlnThrLeuMetLys 137
    |||||.....|||
Db 412 TCTGACTATATATTAAGCTCTGTGAAGATGACAGTTTGAACAAGAACTATAGAAAA 471
Oy 138 LeuGlnLeuThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeu 157
    |||||.....|||
Db 472 CTACAAAGGTCAAAATTTGATGTCTCTGCGAGATGCCCTTAACTCCCTGTGGAGCTG 531
Oy 158 MetAlaGlnLeuAlaValProPheValLeuThrLeuArgLysSerValGlyAsn 177
    |||||.....|||
Db 532 CTGGCTGAACACTTAACATACCTTCTGTACAGTCTCCGCTTCTGTGTGGCTACACA 591
Oy 178 MetGlnAspSerCysGlyLysLeuProAlaProLeuSerTyrValProValPrometThr 197
    |||||.....|||
Db 592 GTTAGAAGAAATGATGAGGATTTCTGTCCCTCTCCATATGATGATGATGATG 651
Oy 198 GlyLeuThrAspArgMetThrPheLeuGlnArgValLysAsnSerMetLeuSerValLeu 217
    |||||.....|||
Db 652 GAATTAAGTGTCAAAATGATTTTCATGAGAGAGATAAAAAATGATATATATCTTAT 711
Oy 218 PheHisPheTTPLeuGlnAspTyrHisPheTTPGlnGluPheTyrSerLysAla 237
    |||||.....|||
Db 712 TTTGACTTTTGGTTTCAAGCATATCATCTGAAGAAAGTGGACAGTTTATAGTGAAGT 771
Oy 238 LeuGlyArgProThrThrLeuCysGlnThrValGlyLysAlaGlnIleTTPLeuIleArg 257
    |||||.....|||
Db 772 CTAGAGAACCCACTACATATTATTGAGAAATGGGGAAGCTGAATAATGGCTCATTCGA 831
Oy 258 ThrTyrTTPAspPheGlnPheProGlnProTyrGlnProAsnPheGlnPheValGly 277
    |||||.....|||
Db 832 ACCATTTGGGATTTTGAATTTCTCCCATTTCTTACCAAAATGTTGATTTTGGTGAAGA 891
Oy 278 LeuHisCysLysProAlaLysAlaLeuProLysGlnMetGlnAsnPheValGlnSerSer 297
    |||||.....|||
Db 892 CTTCACGTAAACCAAGCAACCTTGCTTACGAAATGGAAGATTTGTGAGAGCTCT 951
Oy 298 GlyLysAspGlyTyrLeuValPheSerLeuGlySerLeuPheGlnAsnValThrGlnGln 317
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Db 952 GGGAGAAATGATTTGTGTGTTTCTGTGGGTCGATGATAGTATACATGTCAAGAA 1011
Oy 318 LysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTTPArgTyr 337
    |||||.....|||
Db 1012 AGTGCACAAATGATTTTCATCAGCCCTGGCCAGATCCCAAAAGCTTATAGAGATTT 1071
Oy 338 LysGlyLysLysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTTPLeuProGln 357
    |||||.....|||

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Db 1072 GATGGCAGAGACCAATACCTTAGTTCACATCTCGACTGATATAGTGTACCCAG 1131
Oy 358 AsnAspLeuGlnGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGly 377
    |||||.....|||
Db 1132 AATGACCTTCTGTGCTATCCCAAAACCAAAAGCTTTATATCTCATGTGTGAAACCAATGCG 1191
Oy 378 IleTyrGlnAlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGln 397
    |||||.....|||
Db 1192 ATCTATAGGCGATCTACCATGGATCCCTTATGTGTGGGCAATCCCTTGTGGGATCA 1251
Oy 398 LeuAspAsnIleAlaHisMetLysAlaLysGlyAlaAlaValGlnIleAsnPheLysThr 417
    |||||.....|||
Db 1252 CATATATACATTTGCTACATATGAAGCCAGAGACCCCTCAGTGTGACATACAGACC 1311
Oy 418 MetThrSerGlnAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLys 437
    |||||.....|||
Db 1312 ATGTCAATAGATGATTTGCTCATATGCAATGAAAGACAGCATTAATGACCTATATATA 1371
Oy 438 GlnAsnAlaMetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArg 457
    |||||.....|||
Db 1372 GAGATATATCATGAATATATCAAGAAATTCATCATGATCAACCGGTGAAGCCCTGATCGA 1431
Oy 458 AlaValPheTTPLeuGlnPheValMetArgHisLysGlyAlaLysHisLeuArgSerAla 477
    |||||.....|||
Db 1432 GCAGCTTCTGGATGAGTTGTGTCATGCGCATTAAGGACCAAGCACTTGGGGTGGCA 1491
Oy 478 AlaHisAspLeuThrTTPPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThr 497
    |||||.....|||
Db 1492 GCCCAACACCTGACCTGATGATCCAGATCCACACCTTGTGATGATATGATCTCTGCGCC 1551
Oy 498 CysValAlaThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPhe 517
    |||||.....|||
Db 1552 TCGGTCGCAATGATATATATATGATACAAAATGTGCTGTTTGTTCGGAAGCTT 1611
Oy 518 AsnLysThrArgLysIleGlnLysArgGln 527
    |||||.....|||
Db 1612 GCCAAACAGAAAGAAAGAAAGGAGT 1641

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RESULT 2
US-09-813-918-1
? Sequence 1, Application us/09813918
? Patent No. 6383789
? GENERAL INFORMATION:
? APPLICANT: WEBSTER, Marion et al.
? TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
? TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
? TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
? FILE REFERENCE: CL001175
? CURRENT APPLICATION NUMBER: US/09/813,918
? CURRENT FILING DATE: 2001-03-22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1413
? TYPE: DNA
? ORGANISM: Human
? US-09-813-918-1

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Alignment Scores:
Pred. No.: 2,21e-158 Length: 1413
Score: 1399.00 Matches: 277
Percent Similarity: 62.83% Conservative: 56
Best Local Similarity: 52.26% Mismatches: 103
Query Match: 49.93% Indels: 94
DB: 4 Gaps: 5

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US-09-784-340-2 (1-527) x US-09-813-918-1 (1-1413)

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Oy 9 ValPheLeuLeuGlnLeuPheCys---ValGlyCysGlyPheCysGlyLysValLeu 27
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Db 44 GTTCTCTGCTGATATACATCTCAGTTGTACTTATGCTCTGGAGCTTGTGAAAAAGTCTG 103

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? EARLIER APPLICATION NUMBER: US 09/285,333
? EARLIER FILING DATE: 1999-04-02
? NUMBER OF SEQ ID NOS: 289
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO: 21
? LENGTH: 391
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-370-838-21

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Pred. No.:	5, 77e-8	Length:	391
Score:	391.00	Matches:	75
Percent Similarity:	72.09%	Conservative:	18
Best Local Similarity:	58.14%	Mismatches:	36
Query Match:	13.95%	Indels:	0
DB:	4	Gaps:	0

US-09-784-340-2 (1-527) x US-09-370-838-21 (1-391)

QY	301	GLYILEVALVALPHESERLEUGLISERLEUPHEGLINSVALITRRGLUGLUSVALAASN	320
Db	3	GGAAFTGGTGTTTCTCTTTGGATGCATGGTCTCAGAAATTCAGAGAAAGAAAGCTGTG	62
QY	321	ILEILEALASERALALEUALAGLILIEPROGLINLYSVALLEUTRPARGTRYLYSGLYLYS	340
Db	63	GGCATGTGTCGTGCTTGGGCAAAATCCCTCAGACAGCTGTGGCGGTACACTGGAC	122
QY	341	LYSPROSERITRLIEUGLYALAASTHARGLEURYSPTRPIIEPROGLINASNAPLEU	360
Db	123	CGACCATGGAATCTTGGCGAACACACGATTACTTTTCAGTGGCTACCCCAAAAGATCTG	182
QY	361	LEUGLYHSIPROLYSTHRLYSALAPHEITHRHISGLYGLYMETASNGLILETRYGLN	380
Db	183	CTTGCTACCCCAAGACCCCGCTGCTTATTCACCATGCTAGTTCCTCAGTGTGAATGAA	242
QY	381	ALALETRYHISGLYVALPROMETVALGLYVALPROILEPHEGLYASPGINLEUASPAN	400
Db	243	AGCATATGCATGGGGGTGCCCATGGTGTGATACCTTATTTGGTGTGATCAGATGACAAAT	302
QY	401	ILEALAHISMETLYSVALYSGLYVALALVALJULILEASNPLEYSTRHMETHRSER	420
Db	303	GCAAAGCCGACGAGAGACTAAAGGGAGCTGGAGTACCTGGAATGCTTTCGAGATGACTTCT	362
QY	421	GLUASPLEULEUARGALALEUARYTHR	429
Db	363	GAAAGTCTAGAAATGCTCTTGAAGAGC	389

RESULT 6
PCT-US92-00282-18
Sequence 18, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435

```

ATTORNEY/AGENT INFORMATION:
NAME: SCOTT WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US92-00282-18

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Read No. 4			
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Read No. 99			
Read No. 100			

US-09-784-340-2 (1-527) x PCT-US92-00282-18 (1-1190)

QY	15	LeuPheGlyVal-----GlyCysGlyPheCysGlyValValLeuValTrrProCys	31
Db	130	CTGCTGTGTGTGCGTGGGGCCACAGTGGTGTCCATCTGTGGAAAGATACTGTTGATCCCA	185
QY	32	AspMetSerHisTrpLeuAsnValLysValIleuGluGluLeuIleValArgGlyHis	51
Db	190	GATGGACGCCACTGGCTGAGCATCTTGGGGCCATCCAGACAGCTGCAGACAGGGGACAT	249
QY	52	GluValIhrValIleuThrHisSerLysProSerIleuIleAspTyrArgLysProSerAla	71
Db	250	GAATAGTGTGCTCAGACA-----CTCAGCCCTGCTTGTATCATCAGACGACGACA	300
QY	72	Leu---LysPheGluValValHisMetProGlnAspTrpThrGluGluAsnGluIlePhe	90
Db	301	TTTTACACCTTGAAGACGTAACCTCTGTGCATCCAAAGGAGAGATGGAAGAAGCTTTT	366
QY	91	ValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTrpGlnSerValIleLysLeu	110
Db	361	GTTAGTGTGGGGCATATGATTTTGGAAATGATCTTCTCTGCAGCCTGTGATCAAAACA	420
QY	111	AsnAspPhePheValGluIleArgGlyThrIleuLysMetLysCysGluSerPheIleTyr	130
Db	421	TACAGAAAATAAAAAAAGAGCTGTGCTATGCTTTTGTCTGGCTGTCTCCACTTACTCAC	486
QY	131	AsnGlnThrLeuMetLysLysLeuGlnGluThrAsnTyrAspValMetLeuIleAspPro	150
Db	481	AACAGAGAGCTCAGTGGCTCTCTCTGGCAGAAAGCAGCTTGTGATGTCAAGCTGAGGACCT	546
QY	151	ValIleProCysGlyAspLeuMetAlaGluLeuLeuAlaValProPheValLeuThrLeu	170
Db	541	TTCCTCTTGCACCCCATGTGTGGCCAGTACATGTCTCTTGCCTCCCATGTATCTTCTTG	600
QY	171	ArgIleSerValGlyLysAsnMetGluArgSerCysGlyLysLeuProAlaProLeuSer	190
Db	601	CAT---GCAGTGCATGACGCTTGAATTGAGGCTACCCACAGTGCCCCAACCCATTCTCC	655
QY	191	TyrValProValProMetThrGlyLeuThrAspArgMetThrPheLeuGluArgValLys	210
Db	658	TACGTGCCACAGCCTCTCTCTCTCATTCACATACATGACACTTCCTCGACAGGGGTAG	712
QY	211	AsnSerMetLeuSerValLeuPheHisPheTrpIleGlnAspTyrAspTyrHisPheTrp	230
Db	718	AACATGTCATTTGCTTTTGCACAGAACTTT---CTGTGCAGCAGTGTTATTTCCCGCAT	774
QY	231	GluGluPheTyrSerLysAlaLeuGlyAlaProThrThrLeuGlyGluThrValGlyLys	250

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Db 310 ATCAAAACAAGAAATTTTTCACCTTGACACCAACTATGCCATTTCATGAGACCCAGATGAA 369
Oy 84 ThrGlu-----GluasnGluIlePheValAsp 92
Db 370 TTTGATGCCCTTGTCGTGGGCGACACACACACTGACTGATCTTGAACAGCAATTTT----- 423
Oy 93 LeuAlaLeuAsnValLeuProGlyLeuSerThrTrpGlnSerValIleIleuLeuAsnAsp 112
Db 424 -----CTGAAAGCATTTTCTAAAGATGATGCAATTTTGGAA--AAATTCA 465
Oy 113 PhePheValGluIleArgGlyThrLeuLysMetMetCysGluSerPheIleIleArgGln 132
Db 466 TCTTGTGCTTTTCATATGAGTCT-----TGTGTGAGACTACTGACATAAAGAG 510
Oy 133 ThrLeuMetCysLysLeuGlnGluThrAsnTyrAspValMetLeuIleAspProValIle 152
Db 511 GCCCTGATCAGGACACCTBAATGCTACTTCTCTGCATGTGGTTTAATAGACCAATTTTAC 570
Oy 153 ProCysGlyAspLeuMetAlaGluLeuLeuAlaValAProPheValLeuThrIleArgIle 172
Db 571 CTCGTGTGGGCGAGTGTGCGCTAACTACTATCAATCTCTGCTGTGTTTTTTGGAG--- 627
Oy 173 SerValGlyGlyAsnMetGluArgSerCysGlyLysLeuProAlaProLeuSerTyrVal 192
Db 628 AACATCTCCATGTGATTTAGACTTTAGCGGACACACAGTCTCCAAATCTCTCTCTATAT 687
Oy 193 ProValAPrometThrGlyLeuThrAspArgMetThrPheLeuGluIleArgValLysAsnSer 212
Db 688 CCTAAGTACTACTAGCACCACATTCAGACACATGACATTCCTCTGCAAGAGGTCAAGAACATG 747
Oy 213 Met-----LeuSerValLeuPheHisPheThrPileGlnAspTyrAspTyrHis 228
Db 748 CTCATACCTCTGGGCGCTGCTACTCTTGCATCTCTTCTGCTCTTAT----- 798
Oy 229 PheTrpGluGluPheTyrSerLysAlaLeuGlyArgProThrThrIleCysGluThrVal 248
Db 799 -----GCAGACCTTGCCCTCGACCTTTTTCAGAGGAGGTGATGAGTGGATCTTCTC 852
Oy 249 GlyLysAlaGluIleTrpLeuIleArgThrTyrTrpAspPheGluPheProGlnProTyr 268
Db 853 AGCCATGCACTGTGTGGCTCTTCCGAGGGGACTTTGTGATGATTAACCCAGGCGCATC 912
Oy 269 GlnProAsnPheGluPheValGlyGlyLeuHisCysLysProAlaLysAlaLeuProLys 288
Db 913 ATGCCAACATGAGTCTTCATTTGGGGGCGATCAACGTGCCAAGGAAGCATATATCAG 972
Oy 289 ---GluMetGluAsnPheValGlnSer 296
Db 973 GTCGGTGTTCGTGCTTCATTCACATCA 999

RESULT 8
PCT-US92-00282-10
: Sequence 10, Application PC/TUS9200282
: GENERAL INFORMATION:
: APPLICANT: OWENS, IDA S.
: APPLICANT: RITTER, JOSEPH K.
: TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
: TITLE OF INVENTION: THEREIN.
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CUSHMAN DARBY & CUSHMAN
: STREET: 1615 L STREET, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20036-5601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/00282
:

```


Db	176	CTGGCTGCTTCCTCCACTGTCCACAGCCCTGGGCTGAGAGTGGAAAGGTGTGGTGGTGGCC	235
Oy	31	CysAspMetSerHisTrpLeuAsnValHisIleLeuGluGluLeuValIleArgly	50
Db	236	ATTTCATGGCACCACCTGGCTGCAGCATGCGGAGAGTCTTCCGGGAGCTCATCCAGAGGC	295
Oy	51	HisGluValThrValLeuThrHisSerLysProSerLeuIleAspTyrArgLysProSer	70
Db	296	CACCAGGACAGTGGTCCACCCAGAGAGGTGAATATGCATCATCAAGAAGAACTTTTTC	355
Oy	71	AlaLeuLysPheGluValValHisMetProGlnAspArgThrGlu-----	85
Db	356	ACCCTGACAACTATGCAATTCGATTCGTGGACCCAGAGATGAATTTGATCGCCATGTGCTGGGC	415
Oy	86	-----GluAsnGluIlePheValAspLeuAlaLeuAsnValLeuPro	99
Db	416	CACACTCAACGTACTTTGAAACAGAACATTTTCTGAAG-----	454
Oy	100	GlyLeuSerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluIleArgly	119
Db	455	-----AAATTTTTCAGAACTATGGCAATGTGCAACATATGCTTTG-----	496
Oy	120	ThrLeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysGln	139
Db	497	GTCATCATAGTCTGTTGTGGAGCTACTCATCAATAAAGAGCCCTGTATCAGCCACTGAT	556
Oy	140	GluThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspMetMetIa	159
Db	557	GCTACTTCCTTGAATGGTGTTTTACAGACCCCGTTATACCTCTGGCGGACATGCTGGCT	616
Oy	160	GluLeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGlu	179
Db	617	AAGTACCTGGTGAATCCTACTGTGTTTTTTTGGAG---AACATTCAGATGATTTTAAAC	673
Oy	180	ArgSerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeu	199
Db	674	TTTTAAGGGCACACAGTGCCTCCAAACCCTTCCTCATATTCCTAGATTACTAACACCAAT	733
Oy	200	ThrAspArgMetThrPheLeuGluValLysAsnSerMet-----LeuSer	215
Db	734	TCAGACCAATGACATTCATGACAAAGGGTCAAGAACATCCTCTACCCCTTGCCCTGTCC	793
Oy	216	ValLeuPheHisPheTrpIleGlnAspTyrAspTyrHisPheTrpGluGluPheTyrSer	235
Db	794	TACATTTGGCATGCTGTTTCTGCTCCTTA-----GCCAGCTTGCTCT	838
Oy	236	LysAlaLeuGlyArgProThrThrLeuCysGluThrValGlyLysAlaGluIleThrLeu	255
Db	839	GAGCTTTTTCAGAGAGAGGTGTCAGTGGTGGATATTTCTCAGTCAGACATCTGTGGCTG	898
Oy	256	IleArgThrTyrTrpAspPheGluPheProGlnProTyrGlnProAsnPheGluPheVal	275
Db	899	TTTCGAGGGGACCTTTGATGATGACCTCCACCGCCATCATGCCACACATGGTCTTCAAT	958
Oy	276	GlyLysLeuHisCysLysProAlaLysAlaLeuProLysGlu---MetGluAsnPheVal	294
Db	959	GG-GGCATCAACGTGTGCCAACAGGAAGCCACTATCTCAGAGTCTGATTTGGTCCTTTCATC	1017
Oy	295	GlnSer 296	
Db	1018	CAATCA 1023	
RESULT 10			
PCT-US92-00282-22			
; Sequence 22, Application PC/TUS9200282			
; GENERAL INFORMATION:			
; APPLICANT: OMENS, IDA S.			
; APPLICANT: RITTER, JOSEPH K			
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION			
; TITLE OF INVENTION: THEREIN.			
; NUMBER OF SEQUENCES: 40			
; CORRESPONDENCE ADDRESS:			

```

? ADDRESS: CUSHMAN DARBY & CUSHMAN
? STREET: 1615 L STREET, N.W.
? CITY: WASHINGTON
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20036-5601
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US92/00282
? FILING DATE: 19920110
? CLASSIFICATION: 435
?
? ATTORNEY/AGENT INFORMATION:
? NAME: SCOTT, WATSON T.
? REGISTRATION NUMBER: 26581
? REFERENCE/DOCKET NUMBER: 91532-PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-861-3000
? TELEFAX: 202-822-0944
?
? TELEX: 6714627 CUSH
?
? INFORMATION FOR SEQ ID NO: 22:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 783 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? MOLECULE TYPE: cDNA
?
? PCT-US92-00282-22
?
?
?
?
? Alignment Scores:
? Pred. No.: 6.04e-25 Length: 783
? Score: 287.00 Matches: 63
? Percent Similarity: 38.89% Conservative: 14
? Best Local Similarity: 31.82% Mismatches: 27
? Query Match: 10.24% Indels: 94
?
? DB: 5 gaps: 1
?
?
?
?
? US-09-784-340-2 (1-527) x PCT-US92-00282-22 (1-783)
?
? QY 330 ProGlnLysValLeuThrPArgTyrGlySgLYrSlySProSerThrLeuGLyAlaAsnThr 349
? ||| :::::::::::::::::::: ||| :::::::::: ||| ::::::::::
?
? Db 93 CCCTCCCAAGGTCCTGTGGCGGTACACGTGGAACCCGACCATGAAATCTTGGCAACAACAGC 153
?
? QY 350 ArgLeuTyrAspTrpIleProGlnAsnAspLeu 361
? ||| :::::::::::::::::::: |||
?
? Db 153 ATACTTGTTAAGTGGCTACCCCAACAGATCTGCTGTGTATGTTGGGGCGATGTGATGTA 212
?
? QY 361 ----- 361
?
? Db 213 TAGGCAACAACAGGGTCAAAATTAGAAAATGGCTTAAGCACAGCTAATCTAAAGATTGT 272
?
? QY 361 ----- 361
?
? Db 273 TGAGCTGAAAAATATTATTAGCAACATATCTCAATGCTTTTATTCTAAGTGGGTATCTC 332
?
? QY 361 ----- 361
?
? Db 333 AACCCACATTTTCTTCGCAAAATTCTGCAAGGGCATGTAGTAACAACAGTCTTTGGA 392
?
? QY 361 ----- 361
?
? Db 393 GTGTTTTCAGAACCTAGATGTGTCCAGCTGTGAACACTGAGATGTAACCTGTCACATCC 452
?
? QY 362 ----- 361
?
? Db 453 TCCCATATTTTGCATCTCAGGTCAGGCCGATGACCCGCTGCTTATATCCACCAAGCTGGTCC 512
?
?
?
? AsnGlyIleTyrGluAlaIleTyrHisSlyValProMetValGlyValProIlePheGly 395
? :::::::::::::::::::: ::::::::::::::::::::
?
? 513 CATGGTGTTTTGAAGCATATGCAAGGGCGTTCGATAGTGATGATAGCCCTGTTGGT 572

```

OY	396	AspGlnLeuAspAspGlnIleAlaHisMetLeuLysGlyAlaAlaValGluIleAspPhe	415
Db	573	GATCGATGAGGAAATGCGCAAAAGCGCATGAGCACTAAGGAGCGTGGAGGACCGCTAAAGTT	632
OY	416	LysThrMetTrpSerGluAspLeuLeuArgLysLeuArgTrpValIleThrAsp	433
Db	633	CTGCAATGAGACTTCGAGAGATTTTGAAATAATGCTCTAAAGCAGTCATCAATGAC	686

```

RESULT 11
PCT-US92-00282-25
Sequence 25, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US92-00282-25

```

Alignment Scores:	
Pred. No.:	8, 71e-24
Score:	281.50
Percent Similarity:	74.19%
Best Local Similarity:	59.14%
Query Match:	10.05%
DB:	5
Length:	1561
Matches:	55
Conservative:	14
Mismatches:	22
Indels:	2
Gaps:	1

US-09-784-340-2 (1-527) x PCT-US92-00282-25 (1-1561)

OY	435	SerTyrLysGluAsnAlaMetArgLeuSerArgIleHisAspGlnProValLysPro	454
Db	269	ACTTCAAGGAGAAATCATATCGCTCTCCAGCTTCCACAAAGAGCCCGGTGGACCG	328
OY	455	LeuAspArgAlaValaPheTrpIleGluPheValaMetArgHisLysGluAlaLysHisLeu	474
Db	329	CTGGACCTGGCGGTCTTGGGTGGAGTTGTGATGAGCGCAAGAGCGCCCACTCG	388
OY	475	ArgSerAlaAlaHisAspLeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPhe	494
Db	389	CGCGCCGACGCCACGACTCACTCGTACAGAGTCACTTCCTTGAGCATTTGGTTTC	446

Oy 495 leleuthrcysvala-Thralialepelephrcysphaleu^{phrcys} 514
 Db 449 cttcttgcgcctgcctgcacacgcttccttcacctttaa^{ttg}tgcctttagccta 508
 Oy 514 sgnlvs---phe^{snlvs}lnlthn^{tr}aglysl^laglyls 525
 Db 509 ccggaaatgcttgcgaa^{aa}aaagcgccgacttaacaaa 545

```

RESULT 12
US-08-942-012B-23
: Sequence 23, Application US/08942012B
: Patent No. 6235278
:
GENERAL INFORMATION:
:
APPLICANT: Miller, Lois K.
:
APPLICANT: Lu, Albert
:
APPLICANT: Dieckes, Peter
:
APPLICANT: Black, Bruce
:
TITLE OF INVENTION: Biological Insect Control Agents Expressing
:
TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
:
FILE REFERENCE: 28-96a
:
CURRENT APPLICATION NUMBER: US/08/942,012B
:
CURRENT FILING DATE: 1997-10-01
:
PRIOR APPLICATION NUMBER: 08/729,606
:
PRIOR FILING DATE: 2000-10-01
:
NUMBER OF SEQ ID NOS: 33
:
SOFTWARE: PatentIn Ver. 2.0
:
SEQ ID NO 23
:
LENGTH: 2025
:
TYPE: DNA
:
ORGANISM: Helicoverpa zea nuclear polyhedrosis virus
:
FEATURE:
:
NAME/KEY: CDS
:
LOCATION: (1320)..(1867)
:
US-08-942-012B-23

```

Alignment Scores:	9.33e-23	Length:	2025
Pred. No.:	274.50	Matches:	121
Score:	41.32%	Conservative:	105
Percent Similarity:	22.12%	Mismatches:	217
Best Local Similarity:	9.60%	Indels:	105
Query Match:	4	Gaps:	19
DB:			

US-09-784-340-2 (1-527) x US-08-942-012B-23 (1-2025)

Oy	5	lysSerAlaLeuValPheLeuLeuLeuGlnIleuPheCysValGlyCysGlyPheCysGly	24
		:::	
Dd	326	AAACAATATACATACATATGTTATTGTTGGTGGTGGTTC -GTCGGTTCGGATGGACGGC	384
Oy	25	Lys -ValLeuValIleTrpProCys - - - AspMetSerHisTrpLeuAsnValLysValIleLe	43
Dd	385	TATCTGTCGGCTTTTCTTCCTTCCTTCGACAGTCATCATGTCACAGTGTTCGACCTTACAC	444
Oy	43	uglIuLeuIleValIarGlyHisGluValThrValLeuThrHisSerLysProSerLe	63
Dd	445	CAATGCTCTGACGCTCCGCGGCCAATACATATGCAATTCACA - - - - -	487
Oy	63	uIleAsPTyrArgLysProSerAlaLeuLeuPheGluValValHisMetProGlnsPar	83
Dd	488	- - - - - CCGTTTCCCACTAG - - - - - AAAAAGCATTC	513
Oy	83	gThrGIuGIuAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGlyLeuSerTh	103
Dd	514	ATCCACAGCTACAGATGTCACAGTTCGTCGCAAAATATATTTTAAACGCTTTCGGA	573
Oy	103	rTrpGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyTrpIleuLysMe	123
Dd	574	CCGATCTAGACGTGTTCACAAACGAGGCGTTATTTCGGA - - - - - ACGTCCACGT	624
Oy	123	tMetCysIuSerPheIle - - - - - TyrAsnGlnThrIle	134
Dd	625	GACGCGCTGCATTTACATCAGTCTAGAACACATGTTAGTTGATCAATTTCTCTGGGAGAG	684

Oy	134	umelLysylsLeuclnluLthrIsn-----TyrAspValMetLeuIleAspProValIl	152
Db	665	TTGACGAAATATGATTCGAATTCGAACAAATGTTTTGCGATTGTTGGTCACCGAAGCCCTTCT	744
Oy	152	eProCysglYAspLeuMetLacIleuLeuAla---ValProPheValLeuThrLeuAr	171
Db	745	AGATTATCCCTGGTGTGTTTTCCGATTGTTGGCCGATGTCCT-----GTCAATACA	795
Oy	171	gIleSerValglYglYAsnMetgluarYserCysglYIleuProAlaProLeuSerTy	191
Db	796	AATTTCGTCGGGTACACGCTTTGGCGGCAAAATTTTGAGACAAATGGAGACC--GTAGCGG	852
Oy	191	rValProValProMetThrIglYLeu-----	199
Db	853	ACATCCCATTTACTATCCAAATTTGGTGGCCCAAAATTTCAAAATTTAAACGTTTGGGA	912
Oy	200	-----ThrAspArgMetThrPheLeuGlu-----ArgValLysAs	211
Db	913	GATATATACGGAAATCTATACAGAACTGGTGCTGTACTTGGAAATTTGCTGTTTGGCCGA	972
Oy	211	nSerMetLeuSerValLeuPheHisPheTrpIleGlnAspTyAspTyHisPheTrpGl	231
Db	973	CGAACAAACATTAATGCTTGGCAT-----	997
Oy	231	uGluPheTySerLysAlaLeuclYlArpThrThrLeuCysgluThrVal--GlyLy	250
Db	998	-----CAATTCGACCAACAAACGCCACCGCCAGTGAAGAACTCGACACAGC	1041
Oy	250	sAlaGluuIleTrpLeuLeuArgThrTyrrTrpAspPheGluPheProGlnProTyGlnPr	270
Db	1042	CGTTCAATTAATGTTTGTGTGAATACGCAATCCGCTGTTGTGTAATATACAGACGATACGCC	1101
Oy	270	oAsnPheGluPheValglYglYLeuHisCysLysProAlaLysAlaLeuProTyGluMe	290
Db	1102	GAGGTACAAATATTGGGAGAGCTACACTCTGATTCGAACAAATGATGTGACGAACACGA	1161
Oy	290	tGlu-----AsnPheValGln-----SerSerGlyIAspGlyIleValIAlp	305
Db	1162	AACGATGACACTAATTAATTTGATGCAATTTTAATTAATCTACAAACGGTGCTGATAGCT	1221
Oy	305	eSerLeuGlySer-----LeuPheGlnAsnVa	314
Db	1222	GAGTTCGCGTACGCTATATACAGCTTTACAGATGACGACGAGAAATTTCTGTGTGAATTTAT	1281
Oy	314	lThrGluGluLysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValIe	334
Db	1282	AACA-----GTTTCAAGCACTTATACCTATATATATTT	1314
Oy	334	uTrpArgTyLysGly--LysLysProSerThrIleuGlyAlaAsnThrArgLeuTyAs	353
Db	1315	GTGGAAACACGAGATGGAATGCCCATGGAACACGTAATGCTTAATAATGTTGTGCACAAAC	1374
Oy	353	pTrpIleArgProGlnAsnAspLeuLeuGlnHisProLysThrLysAlaPheIleThrHisGl	373
Db	1375	TTGGCTGCGCGAACACCATATATTGAACACACAAATGATGATGTCATTGTTGTTGATCCAAAG	1434
Oy	373	yGluMetAsnGlyIleTyTrgluaIalIeTyHisGlyValAPrometValGluValProIl	393
Db	1435	CGGAATGACGACAAAGGACGACAAACGATCCAGCGTTGTGTACCACTATATGGAAATCCGTT	1494
Oy	393	ePheGlyAspGlnLeuAspAsnIleAlaHisMetLysAlaLysGlyAlaAlaValaGluIl	413
Db	1495	TATGACGCGACCAACGATACATACCAATAAATACGAAGAATCGGAATCGGACGACACCT	1554
Oy	413	eAsnPheLysThrMetThrSerGluAspLeuLeuAlaGluAlaLeuAla-----ThrValIl	431
Db	1555	CGATCCCGTAAACGCTGCACAACTATATTTGGTGTGCTGCGCTTTAGATGTACACCGTCAA	1614
Oy	431	eThrAspSerSerTyLysGluAsnAlaMetArgLeuSerArgIleHisHisAspGlnPr	451
Db	1615	CACAAAGAGTGCCTACACACATATATATTAAGACATTGAATCGTTCCACTAATTTATGCAAC	1674
Oy	451	oValLysProLeuAspArgAlaValAlaPheTrpIleGluPheValMetArgHisLysGlyAl	471

```

Db      1675   ACGGAACCTTATGGAAAAAGGCACATCTGTGACACAGAACATGTAATTGATTAATGTTAAAAA    1730
Oy      471     alyshtleaurgerseAliahtlahtAsrpleuthrtPrphglnhtstSerlleaspya    491
Db      1735   TCCCATTTTTAAAAAGAAAGGCCGCCAACAGTATGTAATAGCAATAATTATATAGAGTAATF    1790
Oy      491     lileglyPheuleauthr    497
Db      1795   CATGTCCTCCTTATTAACG    1813

RESULT 13
PCT-US92-00282-8
; Sequence 8, Application PC/RUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; APPLICANT: RITTER, JOSEPH K.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, MATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ. ID NO.: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1219 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US92-00282-8

Alignment Scores:
Pred. No.:          7e-23           Length:         1219
Score:              272.50          Matches:         98
Percent Similarity: 46.67%          Conservative:    70
Best Local Similarity: 27.22%       Mismatches:     138
Query Match:        9.73%           Indels:         56
DB:                 5               Gaps:           10

US-09-784-340-2 (1-527) x PCT-US92-00282-8 (1-1219)

Oy      6      SerialaleualPhreuleuleInleuPhecysValglCyseclYphycsglyls    25
Db      230   GCAGAGGGTTCTTCTTGACACACTTGGGGCATGGTTGAGGT-----GACAAG    297
Oy      26     ValleunAlTrpproCsaspmetserhtStrpleuasValylsVallleuglu    45
Db      298   CTGCTGGTGGCCCTCAGAGACGGAAGCCACTGCTTAGATGAAGATATAGTTAGGTT    357
Oy      46     lleullevalaArglunlsguilalThruVlleuThrhIsertlysBroserleuileasp    65

```

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Db 358 CTCAGTACCGGGGCTCATGATTTAGTGGTGGCTGAGTAAATTTGCTTTGAA 417
Qy 66 TTTATGlyProSerAlaLeuLysPheGluValAlaHisMetProLinsparGlyIlu 85
Db 418 GAATCCAAATACATACACAGAGAAA-----ATCTATCCAGTGGCCATGATACAGAGAG 471
Qy 86 -----GluAsnGluIlePheValAlaPheValAlaLeuAsnVal 97
Db 472 CTGAGACACCGTTACCATATTTGGAAACAATCACTTTCTGAGGATCCCTCAACT 531
Qy 98 LeuProGlyLeu-SerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluI 117
Db 532 GCTCCCTCAGACAGATACAGAAATACATGATTGATGGCCCTGATACATCAAC-- 589
Qy 117 eArgGlyThrLeuLysMetMetCysGlnSerPheIleTyrAsnGluThrLeuMetLys 137
Db 590 -----TCCAGACCCCTCCCTCAGAGACAGGACACCCCTGAACCT 627
Qy 137 sLeuGlnGluThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAsp 157
Db 628 CTTTAAAGAGAGCAAGTTTGTGCTTTTCACAGACCCAGCCCTTACCTGCGGTGAT 687
Qy 157 uMetAlaGluLeuAlaValProPheValLeuThrLeuArgLieserValGlyLys 177
Db 688 CCTGGC-GAGTATTTGGCCCTACCATCTGTCTACCTCTTCAAG--GGTTTCCGCTTC 743
Qy 177 nMetGluArgSerCysGlyLysLeuProAlaProLeuSerTyrValProValPromet-T 197
Db 744 CTTGAGACATACATTCACAGACAGACCCAGACCCGTGCTCACAATCCCCAGGTACA 803
Qy 197 hrGlyLeuThrAspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerVal 216
Db 804 CAAGTTTTCAGACACATGACTTTTCCACAGAGGCGGACCTCTCTTAAATTTGT 863
Qy 217 -----LeuPheHisPheTrpIleGlnAspTyrAspTyrHisPheTrpGluI 233
Db 864 TGGAGCCCTATCTATTTATTTGTCTGTTTCAAGTAT-----GAGAGAC 908
Qy 233 heTyrSerLysAlaLeuGlyArgProThrThrLeuCysGlyThr-ValGlyLysAlaGlu 252
Db 909 TCGCATCAGACGTCTCTCAAGAGAGATGAGATATCATCCTTATATCATGAGGTCTCT 968
Qy 253 IleTrpLeuIleArgThrThrTrpAspPheGluPheProGlnProTyrGlnProAsn 272
Db 969 GTTTGGCTGTATGATATGATCATCTTGTCTGATATCCTAGGCGCGTATGCCACACG 1028
Qy 273 GluPheValGlyLeuHisCysLysProAlaLysAlaLeuProLysGluMetGluAsn 292
Db 1029 TC-TTCATTTGGAGGTATCAACTGTAAAGAGAGACCTGTCTCAGGTGGTGGTTTA 1087
Qy 293 pheValGlnSerSerGlyLysAspGlyIleValPheSerLeuGlySerLeuPheGln 312
Db 1088 TTTCTTTTGGCTGCC-----TTGTTTCTTCCAGGCTCTCTCTC--- 1126
Qy 313 AsnValThrGluGluLysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGln 332
Db 1127 -----CCTACATCTTGGCTCTTACAGCCAGACGCTGCTGGAGG 1168
Qy 333 ValLeuTrpArgTyrLysGlyLysProSerThrLeuGlyAlaAsnThrArg 350
Db 1169 ATTCTCTGGAGACGGTGGG-----GGAAGGATATACCCGC 1204

```

RESULT 14
PCT-US92-00282-12

Sequence 12, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN

```

STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1197 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US92-00282-12

Alignment Scores:
Pred. No.: 8,96e-23 Length: 1197
Score: 271.50 Matches: 90
Percent Similarity: 44.51% Conservative: 52
Best Local Similarity: 28.21% Mismatches: 112
Query Match: 9.69% Indels: 67
DB: Gaps: 10

US-09-784-340-2 (1-527) x PCT-US92-00282-12 (1-1197)
Qy 24 GlyLysValLeuValIleProCysAspMetSerHisTrpLeuAsnVal---LysValIle 42
Db 313 GGAAGGCTGTGGTGGTGGCCACTGATGCGACCCCTGGTC-TCAATCATGCGGAGGCC 371
Qy 43 LeuGluGluLeuIleValArgGlyHisGluValThrValLeuThr----- 57
Db 372 TTGCGGAGCTCCATGCGCAGAGGCGCAGCGGCGTCTCTCACCCACAGAGTGAATAG 431
Qy 58 HisSerLysPro-----SerLeuIleAspTyrArgLysProSerAlaLeuLys 73
Db 432 CACATCAAGAGAGAAATTTTTCACCTGACAGCCTATCTGTTCATGAGCCAGAG 491
Qy 74 -----PheGluValAlaHisMetPro 80
Db 492 GAATTTGATCGCTTACCGCTGGCTACACTCAAGGCTTTTGAAACAAGAACTTCTCG 551
Qy 81 GlnAspArgThrGluGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
Db 552 AAGAGATTTCTAGAGATGCGCAATATTAACAATGATCTTTG----- 596
Qy 101 LeuSerThrTrpGlnSerValIleLysLeuAsnSphPhePheValGluIleArgGlyThr 120
Db 597 -----GCC 599
Qy 121 LeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
Db 600 CTTCAATAGGTGTGTGTGAGACTACTGATATATAGAGCCCGTGAACAGCAGCCTGAATGCT 659
Qy 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
Db 660 ACTTCCTTGATGTGTGTTTAACAGAGACCCGTTAACCCTGTGTGGCGGCGGTGCTAG 719

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